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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 18, 2003, 13:30:07 ; Search time 28.3382 Seconds
(without alignments)
2457.601 Million cell updates/sec

Title: US-09-807-933B-7
Perfect score: 1826
Sequence: 1 MKFTVAITSIAVALALSSSA.....TPKEVTC²AE¹LTTRSCERK 338

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues
Total number of hits satisfying chosen parameters: 671580

```

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0

```

```
Database :
SPREMBL_21:*
1:  sp archaea:*
2:  sp bacteria:*
3:  sp fungi:*
4:  sp human:*
5:  sp_invertebrate:*
6:  sp_mammal:*
7:  sp_mhc:*
8:  sp_organellae:*
9:  sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp Vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriap:*
17: sp_archaeap:*
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	785.5	43.0	220	14	Q9JH84	Q9JH84 unclassified
2	784.5	43.0	219	14	Q9JH92	Q9JH92 unclassified
3	783.5	42.9	219	14	Q9JH91	Q9JH91 unclassified
4	780.5	42.7	219	14	Q9JH89	Q9JH89 unclassified
5	779.5	42.7	219	14	Q9JH87	Q9JH87 unclassified
6	772.5	42.3	219	14	Q9JH90	Q9JH90 unclassified
7	769.5	42.1	217	14	Q9JH95	Q9JH95 unclassified
8	766.5	42.0	219	14	Q9JH83	Q9JH83 unclassified
9	764.5	41.9	219	14	Q9JH86	Q9JH86 unclassified
10	762.5	41.8	221	14	Q9JH94	Q9JH94 unclassified
11	759.5	41.6	219	14	Q9JH88	Q9JH88 unclassified
12	755.5	41.4	220	14	Q9JH93	Q9JH93 unclassified
13	750	41.1	218	14	Q9JH85	Q9JH85 unclassified
14	745.5	40.8	220	14	Q9JH96	Q9JH96 unclassified
15	718	39.3	305	3	Q9J782	Q9J782 hemicola gr
16	688	37.7	410	3	Q9P868	Q9P868 ptyomaca e

17	645	35.3	227	3	093763	humicola gr
18	560	30.7	242	5	097401	phaeodon coc
19	559.5	30.6	271	3	09UV93	09uyh3 alternaria
20	383.5	21.0	112	14	09UY99	09jh89 unclassified
21	371.5	20.3	112	14	09UY98	09jh88 unclassified
22	371.5	20.3	112	14	09UYA2	09jha2 unclassified
23	368.5	20.2	112	14	09UYA0	09jha0 unclassified
24	365.5	20.0	112	14	09UYA1	09jha1 unclassified
25	350	19.2	111	14	09UY97	09jhb7 unclassified
26	269.5	14.8	476	3	09C189	09c189 humicola in
27	233.5	12.8	471	3	09C8X8	09c8ye trichoderma
28	232	12.7	439	3	092401	092401 agaricus bl
29	230	12.6	439	3	09B893	09B893 agaricus bl
30	229.5	12.6	345	3	09BZ17	09Bz17 penicillium
31	220.5	12.1	457	3	093837	093837 acremonium
32	220.5	12.1	493	3	09P8B0	09P8d0 trichoderma
33	205.5	11.3	408	3	09H8Z2	09H8z2 panerochae
34	205	11.2	197	3	09P7F1	09P7f1 schizosacch
35	202.5	11.1	408	3	09HEZ1	09Hez1 panerochae
36	199.5	10.9	444	3	096VU2	096vU2 lentinula e
37	198	10.8	410	3	012665	012665 penicillium e
38	195	10.7	460	3	002321	002321 panerochae
39	194	10.6	443	3	09C1R4	09c1r4 lentinula e
40	190.5	10.4	418	3	0938J3	0938j3 trichoderma
41	182.5	10.0	823	3	074203	074203 panerochae
42	181.5	9.9	389	3	09C3J8	09c3J8 volvariella
43	179.5	9.8	823	3	09URP5	09urp5 panerochae
44	177.5	9.7	802	3	08TG6	08tg6c panerochae
45	174.5	9.6	533	5	09TY14	09ty14 caenothabdi

ALIGNMENTS

RESULT 1

ID	09JH84	PRELIMINARY;	PR1;	220 AA.
AC	09JH84;			
DT	01-OCT-2000 (TReMBLrel. 15, Created)			
DT	01-OCT-2000 (TReMBLrel. 15, Last sequence update)			
DT	01-MAR-2002 (TReMBLrel. 20, Last annotation update)			
DE	Family 45 cellulase homologue.			
OS	unclassified eukaryotes.			
OC	Eukaryota.			
OX	NCBI_TaxID=42452;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	Onocho K., Onkuma M., Moriya S., Kudo T.;			
RT	"Diverse genes of family 45 cellulase homologues of the symbiotic			
RT	proteins in the hindgut of termite <i>Reticulitermes speratus</i> ."			
RL	Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; AB045179; BAA98049.1; -.			
DR	HSSP; P43316; 2ENG.			
DR	InterPro: IPR000334; GH 45.			
DR	Pfam; PF02015; Glyco_hydro_45.1.			
DR	PROSITE; PS01140; GLYCOSYL_HYDROL_F45; UNKNOWN.1.			
QO	SEQUENCE 220 AA; 23274 MW; 26AF5357512EA061 CAC64;			

	Query Match	Similarity	Score	DB	Length
Best Local	43.0%	66.7%	785.5	12	220
Matches	136	Conservative	28	Mismatches	37
				Indels	3
				Gaps	2
Qy	136	SGSTTRTWDCCKASCSWPKASVTVPTDTCASNGISLIDAN--AOSGCNGNGFMCCNNQ	193		
Db	17	SGRTRRWDCCKASCAWEKKAATVQPVDTGCKDGTTRLASNDITYKSSCDGDDGYVCYDQA	76		
Qy	194	PWAVNDELANGFAAASITAGSNEAGCCGCELTFTSGAASGRKRVVQVTTNTGGDLSNHF	253		
Db	77	PWAVNDVAVYFAAAACCG--GETGACNCCEYELFTTSGVNVKSKRVVQVTTNTGGDLSNQF	135		
Qy	254	DLQMPGGVGIVFNCACAMQMGAPNDMGARVGVGSVSPSCALPSALQGGCKMRPWPFNQS	313		
Db	136	DLALPGGVGIVNCTQGSAPALGQMSRGGVGSRSRSCSLPGLQAGCMRPFWPFDNA	195		

QY 314 DNPTMTFKVTCPAELITRSGCER 337
 DB 196 DNPSINFNVTCPSSELTAKTCKR 219

RESULT 2

Q9JH92 PRELIMINARY; PRT; 219 AA.

AC Q9JH92; TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, last sequence update)
 DT 01-MAR-2002 (TREMBLrel. 20, last annotation update)
 DE Family 45 cellulase homologue.
 OS unclassified eukaryotes.
 OC Eukaryota.
 OX NCBI_TaxID=42452;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Ohtoko K., Ohkuma M., Moriya S., Kudo T.;
 RT "Diverse genes of family 45 cellulase homologues of the symbiotic
 RT protists in the hindgut of termite Reticulitermes speratus."
 RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB045171; BAA98041.1; -
 DR HSSP; P43316; ZENG.
 DR InterPro; IPR000334; GH_45.
 DR Pfam; PF02015; Glyco_hydro_45; 1.
 DR PROSITE; PS01140; GLYCOSYL_HYDROL_F45; UNKNOWN_1.
 SQ SEQUENCE 219 AA; 23001 MW; 5F2EB81A6DE926CE CRC64;

Query Match 43.0%; Score 784.5; DB 14; Length 219;

Best Local Similarity 66.2%; Pred. No. 1.5e-42; Indels 3; Gaps 2;
 Matches 135; Conservative 29; Mismatches 37;

QY 136 SGGTTRVWDCCCKASCMPGKASVTPVDTCAISNGISLIDAN--AQSGCNGNGFMGNNQ 193
 DB 16 SGRTRVWDCCCKASCAMEKKAATVQPVDTCAKDGTRVANSNDTVKSCDDGGEGMCTDQA 75
 QY 194 PMAVNDLAYGPAASISAGSNEAGMCCGCELTFTSGAASGKRVVQVNTGTGDLGSHNF 253
 DB 76 PMAVNDLAYGPAASISAGSNEAGMCCGCELTFTSGAASGKRVVQVNTGTGDLGSHNF 134
 QY 254 DLQMPGGVGIFNGCAQMGAPNDMGARYGVSSVSDCASLPSALQAGCKRRNMFNKS 313
 DB 135 DLAIPEGVGIVNGCTQAGAPSDMGARYGVSSVSDCASLPSALQAGCKRRNMFNKS 194
 QY 314 DNPTMTFKVTCPAELITRSGCER 337
 DB 195 DNPSINFNVTCPSSELTAKTCKR 219

RESULT 3

Q9JH91 PRELIMINARY; PRT; 219 AA.

AC Q9JH91; TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, last sequence update)
 DT 01-MAR-2002 (TREMBLrel. 20, last annotation update)
 DE Family 45 cellulase homologue.
 OS unclassified eukaryotes.
 OC Eukaryota.
 OX NCBI_TaxID=42452;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Ohtoko K., Ohkuma M., Moriya S., Kudo T.;
 RT "Diverse genes of family 45 cellulase homologues of the symbiotic
 RT protists in the hindgut of termite Reticulitermes speratus."
 RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB045172; BAA98042.1; -
 DR HSSP; P43316; ZENG.
 DR InterPro; IPR000334; GH_45.
 DR Pfam; PF02015; Glyco_hydro_45; 1.
 DR PROSITE; PS01140; GLYCOSYL_HYDROL_F45; UNKNOWN_1.

SQ SEQUENCE 219 AA; 23126 MW; A712EF3F3CAB041C CRC64;

Query Match 42.9%; Score 783.5; DB 14; Length 219;
 Best Local Similarity 66.2%; Pred. No. 1.8e-42;
 Matches 135; Conservative 31; Mismatches 35; Indels 3; Gaps 2;

QY 136 SGGTTRVWDCCCKASCMPGKASVTPVDTCAISNGISLIDAN--AQSGCNGNGFMGNNQ 193
 DB 16 SGRTRVWDCCCKASCAMEKKAATVQPVDTCAKDGTRVANSNDTVKSCDDGGEGMCTDQA 75
 QY 194 PMAVNDLAYGPAASISAGSNEAGMCCGCELTFTSGAASGKRVVQVNTGTGDLGSHNF 253
 DB 76 PMAVNDLAYGPAASISAGSNEAGMCCGCELTFTSGAASGKRVVQVNTGTGDLGSHNF 134
 QY 254 DLQMPGGVGIFNGCAQMGAPNDMGARYGVSSVSDCASLPSALQAGCKRRNMFNKS 313
 DB 135 DLAIPEGVGIVNGCTQAGAPSDMGARYGVSSVSDCASLPSALQAGCKRRNMFNKS 194
 QY 314 DNPTMTFKVTCPAELITRSGCER 337
 DB 195 DNPSINFNVTCPSSELTAKTCKR 219

RESULT 4

Q9JH89 PRELIMINARY; PRT; 219 AA.

AC Q9JH89; TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, last sequence update)
 DT 01-MAR-2002 (TREMBLrel. 20, last annotation update)
 DE Family 45 cellulase homologue.
 OS unclassified eukaryotes.
 OC Eukaryota.
 OX NCBI_TaxID=42452;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Ohtoko K., Ohkuma M., Moriya S., Kudo T.;
 RT "Diverse genes of family 45 cellulase homologues of the symbiotic
 RT protists in the hindgut of termite Reticulitermes speratus."
 RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB045174; BAA98044.1; -
 DR HSSP; P43316; ZENG.
 DR InterPro; IPR000334; GH_45.
 DR Pfam; PF02015; Glyco_hydro_45; 1.
 DR PROSITE; PS01140; GLYCOSYL_HYDROL_F45; UNKNOWN_1.
 SQ SEQUENCE 219 AA; 23033 MW; CA295CABDF393195 CRC64;

Query Match 42.7%; Score 780.5; DB 14; Length 219;
 Best Local Similarity 64.2%; Pred. No. 2.8e-42;
 Matches 131; Conservative 33; Mismatches 37; Indels 3; Gaps 2;

QY 136 SGGTTRVWDCCCKASCMPGKASVTPVDTCAISNGISLIDAN--AQSGCNGNGFMGNNQ 193
 DB 16 SGRTRVWDCCCKASCAMEKKAATVQPVDTCAKDGTRVANSNDTVKSCDDGGEGMCTDQA 75
 QY 194 PMAVNDLAYGPAASISAGSNEAGMCCGCELTFTSGAASGKRVVQVNTGTGDLGSHNF 253
 DB 76 PMAVNDLAYGPAASISAGSNEAGMCCGCELTFTSGAASGKRVVQVNTGTGDLGSHNF 134
 QY 254 DLQMPGGVGIFNGCAQMGAPNDMGARYGVSSVSDCASLPSALQAGCKRRNMFNKS 313
 DB 135 DLAIPEGVGIVNGCTQAGAPSDMGARYGVSSVSDCASLPSALQAGCKRRNMFNKS 194
 QY 314 DNPTMTFKVTCPAELITRSGCER 337
 DB 195 DNPSINFNVTCPSSELTAKTCKR 219

RESULT 5

Q9JH87 PRELIMINARY; PRT; 219 AA.

AC Q9JH87; TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, last sequence update)

DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
 DT 01-MAR-2002 (TReMBLrel. 20, Last annotation update)
 DE Family 45 cellulase homologue.
 OS unclassified eukaryotes.
 OC Eukaryota.
 NX NCBI_TaxID=42452;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Ohtoko K., Ohkuma M., Moriya S., Kudo T.;
 RT "Diverse genes of family 45 cellulase homologues of the symbiotic
 RT protists in the hindgut of termite Reticulitermes speratus.";
 RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB045176; BAA98046.1; -
 DR HSSP; P43316; 2ENG.
 DR InterPro; IPR000334; GH 45.
 DR Pfam; PF02015; Glyco_hydro_45.1.
 DR PROSITE; PS01140; GLYCOSYL_HYDROL_F45; UNKNOWN 1.
 SQ SEQUENCE 219 AA; 23134 MW; 4BDEF4E9AC772D CRC64;

Query Match 42.7%; Score 779.5; DB 14; Length 219;
 Best Local Similarity 63.0%; Pred. No. 3.2e-42;
 Matches 133; Conservative 35; Mismatches 40; Indels 3; Gaps 2;

QY 129 ISGKSGSGSTTRVWDCCCKASGWPGRKASVTGPVDTCAISNGISLIDAN--AOSGCGNGANG 186
 DB 9 ISWLSADSGRTTRVWDCCCKSGCGWEKXANVDKPIDTCAKQDTRVANSNDTVKSGCDGDDG 68
 QY 187 FMCNNNDPMAVNDLAVGFAAASAGSNEAGWCCGCELTFTSGAASGKRVVQVNTTGG 246
 DB 69 FMCQDQTFPQVSDLSYGFAPAAACCG-GEAGACCGCELTFTSPVNGKRVVQVNTTGG 127
 QY 247 DLGSHFDLQMPGGVGIFFNGCAQWGAQNDGARYGVSVDCASLPDLAQGCKMR 306
 DB 128 DLGSHFDLQMPGGVGIFFNGCAQWGAQNDGARYGVSVDCASLPDLAQGCKMR 187
 QY 307 FMPKNSDNPMTFKEVTCPAELTTRSGCER 337
 DB 188 FDFWQNDNPISNFSQVSCPELIATKTCNR 218

RESULT 6
 Q9JH90 PRELIMINARY; PRT; 219 AA.
 AC Q9JH90;
 DT 01-OCT-2000 (TReMBLrel. 15, Created)
 DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
 DT 01-MAR-2002 (TReMBLrel. 20, Last annotation update)
 DE Family 45 cellulase homologue.
 OS unclassified eukaryotes.
 OC Eukaryota.
 NX NCBI_TaxID=42452;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Ohtoko K., Ohkuma M., Moriya S., Kudo T.;
 RT "Diverse genes of family 45 cellulase homologues of the symbiotic
 RT protists in the hindgut of termite Reticulitermes speratus.";
 RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB045173; BAA98043.1; -
 DR HSSP; P43316; 2ENG.
 DR InterPro; IPR000334; GH 45.
 DR Pfam; PF02015; Glyco_hydro_45.1.
 DR PROSITE; PS01140; GLYCOSYL_HYDROL_F45; UNKNOWN 1.
 SQ SEQUENCE 219 AA; 23037 MW; 372E016415530A9A CRC64;

Query Match 42.3%; Score 772.5; DB 14; Length 219;
 Best Local Similarity 63.7%; Pred. No. 8.8e-42;
 Matches 130; Conservative 32; Mismatches 39; Indels 3; Gaps 2;
 QY 136 SGSTTRVWDCCCKASGWPGRKASVTGPVDTCAISNGISLIDAN--AOSGCGNGANGPCCNNQ 193
 DB 16 SGTTRVWDCCCKSGCGWEKXANVDKPIDTCAKQDTRVANSNDTVKSGCDGDFMVCYDQ 75
 QY 194 PMAVNDLAVGFAAASAGSNEAGWCCGCELTFTSGAASGKRVVQVNTTGGDLGSHNF 253

DB 76 PMQVSDLSYGFAPAAACCG-GEAGACCGCELTFTSPVNGKRVVQVNTTGGDLGSHNF 134
 QY 254 DLQMPGGVGIFFNGCAQWGAQNDGARYGVSVDCASLPDLAQGCKMRPMPKNS 313
 DB 135 DLQMPGGVGIFFNGCAQWGAQNDGARYGVSVDCASLPDLAQGCKMRPMPKNS 194
 QY 314 DNPMTFKEVTCPAELTTRSGCER 337
 DB 195 DNPISNFKCPELIATKTCNR 218

RESULT 7
 Q9JH95 PRELIMINARY; PRT; 217 AA.
 AC Q9JH95;
 DT 01-OCT-2000 (TReMBLrel. 15, Created)
 DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
 DT 01-MAR-2002 (TReMBLrel. 20, Last annotation update)
 DE Family 45 cellulase homologue.
 OS unclassified eukaryotes.
 OC Eukaryota.
 NX NCBI_TaxID=42452;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Ohtoko K., Ohkuma M., Moriya S., Kudo T.;
 RT "Diverse genes of family 45 cellulase homologues of the symbiotic
 RT protists in the hindgut of termite Reticulitermes speratus.";
 RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB045168; BAA98038.1; -
 DR HSSP; P43316; 2ENG.
 DR InterPro; IPR000334; GH 45.
 DR Pfam; PF02015; Glyco_hydro_45.1.
 DR PROSITE; PS01140; GLYCOSYL_HYDROL_F45; UNKNOWN 1.
 SQ SEQUENCE 217 AA; 22796 MW; 660DD1346B3769DB CRC64;

Query Match 42.1%; Score 769.5; DB 14; Length 217;
 Best Local Similarity 64.7%; Pred. No. 1.4e-41;
 Matches 132; Conservative 26; Mismatches 41; Indels 3; Gaps 2;

QY 136 SGSTTRVWDCCCKASGWPGRKASVTGPVDTCAISNGISLIDAN--AOSGCGNGANGPCCNNQ 193
 DB 14 SGTTRVWDCCCKSGCGWEKXANVDKPIDTCAKQDTRVANSNDTVKSGCDGDFMVCYDQ 73
 QY 194 PMAVNDLAVGFAAASAGSNEAGWCCGCELTFTSGAASGKRVVQVNTTGGDLGSHNF 253
 DB 74 PMQVSDLSYGFAPAAASAGSNEAGWCCGCELTFTSGAASGKRVVQVNTTGGDLGSHNF 132
 QY 254 DLQMPGGVGIFFNGCAQWGAQNDGARYGVSVDCASLPDLAQGCKMRPMPKNS 313
 DB 133 DLQMPGGVGIFFNGCAQWGAQNDGARYGVSVDCASLPDLAQGCKMRPMPKNS 192
 QY 314 DNPMTFKEVTCPAELTTRSGCER 337
 DB 193 DNPISNFKCPELIATKTCNR 216

RESULT 8
 Q9JH83 PRELIMINARY; PRT; 220 AA.
 AC Q9JH83;
 DT 01-OCT-2000 (TReMBLrel. 15, Created)
 DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
 DT 01-MAR-2002 (TReMBLrel. 20, Last annotation update)
 DE Family 45 cellulase homologue.
 OS unclassified eukaryotes.
 OC Eukaryota.
 NX NCBI_TaxID=42452;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Ohtoko K., Ohkuma M., Moriya S., Kudo T.;
 RT "Diverse genes of family 45 cellulase homologues of the symbiotic
 RT protists in the hindgut of termite Reticulitermes speratus.";

RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.

DR EMBL; AB045167; BAA98037.1; -;
DR EMBL; AB045166; BAA98036.1; -;
DR HSSP; P43316; 2ENG.
DR InterPro; IPR000334; GH_45.
DR Pfam; PF02015; Glyco_hydro_45; 1.
DR PROSITE; PS01140; GLYCOSYL_HYDROL_F45; UNKNOWN_1.
SQ SEQUENCE 220 AA; 23108 MW; 97738D831BCFA5F3 CRC64;

Query Match 42.0%; Score 766.5; DB 14; Length 220;
Best Local Similarity 64.2%; Pred. No. 2,1e-41;
Matches 131; Conservative 29; Mismatches 41; Indels 3; Gaps 2;

OY 136 SGGTTRYWDCCKASCSMPGKASVTGPVDTCAISNGISLLDAN--AOSGCGNGGEMCNNO 193
DB 17 SGGTTRYWDCCCKSGSGWEAKADVSKPDTCAKDGTTRVANSNDTVKSGCDGDDGMYCYDQT 76
OY 194 PMAVNDELAYGFAAASINAGSNBAGWCCGCELTFTSGAASGKKMYVQVNTGDLGSNHF 253
DB 77 PMGVNDSVALGFPAALAIISGGEKAA-CCNCELTFTSGPVNGKKMTVQVNTGDLGSNOF 135
OY 254 DLQMPGGVGIFNGCAQOMGAPNDQMGARYGVSSVSDCASLPSALOAGCKMRFNMFKN 313
DB 136 DLAIPEGVGIVNGCTAOSGAPADQMSRGVSSSSSCSQLPSELQAGCCMRPDMQNA 195
OY 314 DNPMTFEKVTCPAELITRSGCER 337
DB 196 DNPSIMFNVSCESELIAKTNCR 219

RESULT 9

OJUH86 PRELIMINARY; PRT; 219 AA.

AC OJUH86;
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)
DE Family 45 cellulase homologue.
OS unclassified eukaryotes.
OC Eukaryota.
NCBI_TaxID=42452;
RN
RP SEQUENCE FROM N.A.
RA Ohtoko K., Ohkuma M., Moriya S., Kudo T.;
RT "Diverse genes of family 45 cellulase homologues of the symbiotic
RT protists in the hindgut of termite Reticulitermes speratus";
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB045177; BAA98047.1; -;
DR HSSP; P43316; 2ENG.
DR InterPro; IPR000334; GH_45.
DR Pfam; PF02015; Glyco_hydro_45; 1.
DR PROSITE; PS01140; GLYCOSYL_HYDROL_F45; UNKNOWN_1.
SQ SEQUENCE 219 AA; 23158 MW; ECD68EAB88ED1D1 CRC64;

Query Match 41.9%; Score 764.5; DB 14; Length 219;

Best Local Similarity 62.7%; Pred. No. 2.8e-41;
Matches 128; Conservative 32; Mismatches 41; Indels 3; Gaps 2;

OY 136 SGGTTRYWDCCKASCSMPGKASVTGPVDTCAISNGISLLDAN--AOSGCGNGGEMCNNO 193
DB 16 SGGTTRYWDCCCKSGSGWEAKADVSKPDTCAKDGTTRVANSNDTVKSGCDGDDGMYCYDQT 75
OY 194 PMAVNDELAYGFAAASINAGSNBAGWCCGCELTFTSGAASGKKMYVQVNTGDLGSNHF 253
DB 76 PMGVNDSVALGFPAALAIISGGEKAA-CCNCELTFTSGPVNGKKMTVQVNTGDLGSNOF 134
OY 254 DLQMPGGVGIFNGCAQOMGAPNDQMGARYGVSSVSDCASLPSALOAGCKMRFNMFKN 313
DB 135 DLAIPEGVGIVNGCTAOSGAPADQMSRGVSSSSSCSQLPSELQAGCCMRPDMQNA 194
OY 314 DNPMTFEKVTCPAELITRSGCER 337
DB 195 DNPSIMFNVSCESELIAKTNCR 218

RESULT 10

OJUH94 PRELIMINARY; PRT; 221 AA.

AC OJUH94;
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)
DE Family 45 cellulase homologue.
OS unclassified eukaryotes.
OC Eukaryota.
NCBI_TaxID=42452;
RN
RP SEQUENCE FROM N.A.
RA Ohtoko K., Ohkuma M., Moriya S., Kudo T.;
RT "Diverse genes of family 45 cellulase homologues of the symbiotic
RT protists in the hindgut of termite Reticulitermes speratus";
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB045169; BAA98039.1; -;
DR HSSP; P43316; 2ENG.
DR InterPro; IPR000334; GH_45.
DR Pfam; PF02015; Glyco_hydro_45; 1.
DR PROSITE; PS01140; GLYCOSYL_HYDROL_F45; UNKNOWN_1.
SQ SEQUENCE 221 AA; 23220 MW; BAA9CEB0AC6372 CRC64;

Query Match 41.8%; Score 762.5; DB 14; Length 221;

Best Local Similarity 63.2%; Pred. No. 3.8e-41;
Matches 129; Conservative 34; Mismatches 38; Indels 3; Gaps 2;

OY 136 SGGTTRYWDCCKASCSMPGKASVTGPVDTCAISNGISLLDAN--AOSGCGNGGEMCNNO 193
DB 17 SGGTTRYWDCCCKSGSGWEAKADVSKPDTCAKDGTTRVANSNDTVKSGCDGDDGMYCYDQT 76
OY 194 PMAVNDELAYGFAAASINAGSNBAGWCCGCELTFTSGAASGKKMYVQVNTGDLGSNHF 253
DB 77 PMGVNDSVALGFPAALAIISGGEKAA-CCNCELTFTSGPVNGKKMTVQVNTGDLGSNOF 135
OY 254 DLQMPGGVGIFNGCAQOMGAPNDQMGARYGVSSVSDCASLPSALOAGCKMRFNMFKN 313
DB 136 DLAIPEGVGIVNGCTAOSGAPADQMSRGVSSSSSCSQLPSELQAGCCMRPDMQNA 195
OY 314 DNPMTFEKVTCPAELITRSGCER 337
DB 196 DNPSIMFNVSCESELIAKTNCR 219

RESULT 11

OJUH86 PRELIMINARY; PRT; 219 AA.

AC OJUH86;
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)
DE Family 45 cellulase homologue.
OS unclassified eukaryotes.
OC Eukaryota.
NCBI_TaxID=42452;
RN
RP SEQUENCE FROM N.A.
RA Ohtoko K., Ohkuma M., Moriya S., Kudo T.;
RT "Diverse genes of family 45 cellulase homologues of the symbiotic
RT protists in the hindgut of termite Reticulitermes speratus";
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB045175; BAA98045.1; -;
DR HSSP; P43316; 2ENG.
DR InterPro; IPR000334; GH_45.
DR Pfam; PF02015; Glyco_hydro_45; 1.
DR PROSITE; PS01140; GLYCOSYL_HYDROL_F45; UNKNOWN_1.
SQ SEQUENCE 219 AA; 23030 MW; 179BF1344C6D7024 CRC64;

Query Match 41.6%; Score 759.5; DB 14; Length 219;

Best Local Similarity 62.7%; Pred. No. 5.9e-41;

	Matches	128;	Conservative	31;	Mismatches	42;	Indels	3;	Gaps	2;
Qy	136	SGSTTRRYDDCCCKASCSMPGKASVYTPVUTCAKNSGISLDDAN--AASGCGNGANGFMFCANNO	193							
Db	16	SGKTRRYDDCCCKSGSGEMERKANVDPEIDTCADGTTVAASNDVTYVSGGDDGGTYMCYDT	75							
Qy	194	PMAVNDLALYGFAPAAASINGSNEAGCCGCEYELFTFTSGAAGSKXNVQVYTNNGDLDGSNHF	253							
Db	76	PMQVSDSLSTYFAPAAACCG--GESGACCCGCEYELFTFTSGVNGIGKMTVQITNTGDDLDGSNQF	134							
Qy	254	DLQMPGGGVGI.FNGCAQMGAPPNNDGMYARVGGVSSVSDCASLPSALQAGCKRPFMFPXNS	313							
Db	135	DLAIPGGGVGIYNGCTSSQSGAPADMDGSRVYGGVSSRSRSCSQIPSGLOAGCQWRPFMFAPNA	194							
Qy	314	DNPTMTKEVATCPALFTTRSGGER	337							
Db	195	DNPNINFTNVKCPSEIIAKTNCLR	218							

RESULT 12		PRT; 220 AA.	
ID	Q9JH93	PRELIMINARY;	
AC	Q9JH93;		
DT	01-OCT-2000 (TREMBLrel. 15, Created)		
DT	01-OCT-2000 (TREMBLrel. 15, Last sequence update)		
DT	01-MAR-2002 (TREMBLrel. 20, Last annotation update)		
DE	Family 45 cellulase homologue.		
OC	unclassified eukaryotes.		
OC	Eukaryota.		
OX	NCBI_TaxID=42452;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RA	Ohno K., Ohkuma M., Moriya S., Kudo T.:		
RT	"Diverse genes of family 45 cellulase homologues of the symbiotic		
RT	protists in the hindgut of termite Reticulitermes speratus."		
RL	Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.		
DR	EMBL; AB045170; BAA98040.1; -.		
DR	HSSP; P43316; 2ENG.		
DR	InterPro; IPR000334; GH_45.		
DR	Pfam; PF02015; Glyco_hydro_45; 1.		
DR	PROSITE; PS01140; GLYCOSYL_HYDROL_F45; UNKNOWN 1.		
SQ	SEQUENCE 220 AA; 23091 MW; 35Fl74F9B79C2D65 CRC64;		
Query Match 41.4%; Score 755.5; DB 14; Length 220;			
Best Local Similarity 62.7%; Pred. No. 1.1e-40;			
Matches 128; Conservative 31; Mismatches 42; Indels 3; Gaps 2			
QY	136 SGSTRRYWDCCASGSPWKASVTPDTCASNGISLLDAN--AOSGCMGNGMFCNNQ 193		
DB	17 TGRTRRYWDCCKGSGEMERKANVDPIDTCADGTRVAASNDTVKSGCDGSGGNCYDOS 76		
QY	194 PMAVNDLALAYGFPAASIASGNSNAGWCCGCELTFTSGAAGKKNVQVNTGDLGSHNF 253		
DB	77 PMGVNDSPALGPAALAAVSGESA--CCNCELTFTSGPVGKKVYQVNTGDLGSGNF 135		
QY	254 DLQMPGGVGIFNGCAQWGAPENDMGARVGVSSVSDCASLPSALQACCKWRFMWFKNS 313		
DB	136 DLALPFGGVGIYNGCTAASGAPADMGSRVSGVSSRSBCCQLPSGLQACQWRFDWFGQA 195		
QY	314 DNPMTTFKEVTCPALTLTRSGER 337		
DB	196 DNPSTISFNVVSCPSLTIKTCNR 219		
RESULT 13			
ID	Q9JH85	PRELIMINARY;	PRT; 218 AA.
AC	Q9JH85;		
DT	01-OCT-2000 (TREMBLrel. 15, Created)		
DT	01-OCT-2000 (TREMBLrel. 15, Last sequence update)		
DT	01-MAR-2002 (TREMBLrel. 20, Last annotation update)		
DE	Family 45 cellulase homologue.		
OS	unclassified eukaryotes.		

OC Eukaryota.
OX NCBI_TaxID=42452;
RN [1]
RP SEQUENCE FROM N.A.
RA Ohtoko K., Ohkuma M., Moriya S., Kudo T.;
RT "Diverse genes of family 45 cellulase homologues of the symbiotic
RT protists in the hindgut of termite *Reticulitermes speratus*.";
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AB045178; BAA98048.1; -.
DR HSSP; P43316; JENG.
DR InterPro; IPR000334; GH_45. .
DR Pfam; PF02015; Glyco_hydro_45. 1.
DR PROSITE; PS01140; GLYCOSYL_HYDROL_P45; UNKNOWN 1.
SQ SEQUENCE 218 AA; 22580 MM; A600FFFS990ADD3 CRC64;

	Query Match	41.1%;	Score 750;	DB 14;	Length 218;
	Best Local Similarity	63.1%;	Pred. No. 2,3e-40;		
	Matches	128;	Conservative	34;	Mismatches 39; Indels 2; Gaps 2;
OY	137	GSTRRYWDCCKASCSPGPKASVTGPVDTTCASNIGISLIDANNAQSCC-NGANGFMCNNNPW	195		
		:	:	:	:
Db	17	GRTRRYWDCCCKSGSGMGDKASVSXPVDTCADGTTRTAVATSAKSAACDSGGTYMYCYDQTPR	76		
		:	:	:	:
OY	196	AVNDELAYGPPAASITADSNEAGMCGCYELFTFGAAGSKGWQVQNTNGDGLCSNHFDL	255		
		:	:	:	:
Db	77	AVNDSTIYAIQFPAAAVSAGEKKA-CCTCYELFTFGPVRNGKMTYQVNTINTGDLSSNQFDI	135		
		:	:	:	:
OY	256	QMPPGGVGIFENGCAAQMGAPNDGNAGARYGVSVSDCASLPALQAQCMMRFNMFKNSDN	315		
		:	:	:	:
Db	136	AIPGGGVGYLVNGCTSGGAPADGNGSRGYSRSSSECSQLPSGIQAQGQMFDFWFQADN	195		
		:	:	:	:
OY	316	PTMTKEVETCPABEILTTIRSGCGRK	338		
		:	:	:	:
Db	196	PSITFNEVSCPGDLTKNCRRQ	218		

QY	Q9JH96	PRELIMINARY;	PRT;	220 AA.
ID	Q9JH96			
AC	Q9JH96;			
DT	01-OCT-2000 (TREMBLrel. 15, Created)			
DR	01-OCT-2000 (TREMBLrel. 15, Last sequence update)			
DT	01-MAR-2002 (TREMBLrel. 20, Last annotation update)			
DS	Family 45 cellulase homologue.			
OS	unclassified eukaryotes.			
OC	Eukaryota.			
OX	NCBI_TaxID=42452;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	Ohtoko K., Ohkuma M., Moriya S., Kudo T.;			
RT	"Diverse genes of family 45 cellulase homologues of the symbiotic			
RL	protists in the hindgut of termite Reticulitermes speratus.";			
RL	Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; AB045165; BAA98035.1; ..			
DR	HSSP; P43316; ZENG.			
DR	InterPro; IPR000334; GH_45.			
DR	Pfam; PF02015; Glyco_hydro_45; 1.			
DR	PROSITE; PS01140; GLYCOSYL_HYDROL_F45; UNKNOWN 1:			
DR	SEQUENCE 220 AA; 23148 MW; 4f0652f8e80d6905 CRC64;			
QY	Query Match	40.8%;	Score 745.5;	DB 14; Length 220;
	Best Local Similarity	63.7%;	Pred. No. 4.5e-40;	
	Matches 130;	Conservative 27;	Mismatches 44;	Indels 3; Gaps 2.
QY	136 SGRTRRWDDCKKASCSPGKASVYTPDTCASNGISILDAN--AOSGCGNGGFMWCKNNQ	193		
DB	17 SGRTRRWDDCKKSGCGMEAKADVSKPIDTCKADGTRVASNDPYVKSICDGGEGTYCYDT	76		
QY	194 PWAVNDELAVGFAPAAASLAGSNEAQMCCGCELYELFTSGAASGRKRVQVYTNNGDLSNHF	253		
DB	77 PRAYNDVSAIGFAAALASIGSEKA--CCQCYELFTTSGVNNKMTYQVYTNNGDLSNQF	135		
QY	254 DLQMPGGGVGIFNGCAAQWGAIPNDGWRVGVSSVSDCASLPSALQAGCKWRPNWPNVS	313		

Db 136 DLAIPGGVGIGYNGTAAGAPADWGSRYGVSSSECSQLPSGLQAGCOMRPFDFONA 195
Qy 314 DNEPTMTFKEVTCPAELTTRSGCER 337
Db 196 DNPISNFNVSCPGELIANTNCRR 219

RESULT 15

ID 093782 PRELIMINARY; PRT: 305 AA.
AC 093782;
DT 01-MAY-1999 (T-EMBLrel. 10, Created)
DT 01-MAY-1999 (T-EMBLrel. 10, Last sequence update)
DT 01-JUN-2002 (T-EMBLrel. 21, Last annotation update)
DE Endoglucanase.
GN EGL3.
OS Humicola grisea var. thermoides.
OC Eukaryota; Fungi; Ascomycota; mitosporic Ascomycota; Humicola.
OX NCBI_Taxid=5528;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=IP09854;
RX MEDLINE=99144540; PubMed=9990729;
RA Takashima S., Iikura H., Nakamura A., Hidaka M., Masaki H., Uozumi T.;
RT "Comparison of gene structures and enzymatic properties between two
endoglucanases from Humicola grisea.";
RL J. Biotechnol. 67:85-97(1999).
DR EMBL; AB003107; BAA74956.1; -.
DR HSSP; P43316; 2ENG.
DR InterPro; IPR000254; CBD_fungal.
DR InterPro; IPR000334; GH_45.
DR Pfam; PF00734; CBM_1; 1.
DR Pfam; PF02015; Glyco_hydro_45; 1.
DR ProDom; PD001821; CBD_fungal; 1.
DR SMART; SM00336; fCBD; 1.
DR PROSITE; PS00562; CBD_FUNGAL; 1.
DR PROSITE; PS01140; GLYCOSYL_HYDROL_P45; 1.
SQ SEQUENCE 305 AA; 32174 MW; 28C979D6EDCD771D CRC64;

Query Match

39.3%; Score 718; DB 3; Length 305;

Best Local Similarity 61.7%; Pred. No. 3,4e-38;

Matches 127; Conservative 26; Mismatches 47; Indels 6; Gaps 3;

Qy 134 SSGSSTRYWDCCAKSCSPGKASVYGPVDTCAASNGISLIDANAQGCN-GANGFMGNNN 192
Db 21 AADGKSTRYWDCCKPCSCGMAKKA PVNDVFSNANFORLTFDAKSGCEPGVAVSCADQ 80
Qy 193 QPNAVNDLAYGPAALSTAGSNEAGMCCGCELTFTSGAASGKKWVQVNTGTGDLGSH 252
Db 81 TPNAVNDLPAPGPAALSTAGSNEAGMCCACETELTFTSGPVAKKVVOSTISGDLGSH 140
Qy 253 FDIQMPGGVGIGYNGTAAGAPADWGSRYGVSSSECSQLPSGLQAGCOMRPFDFON 311
Db 141 FDIQMPGGVGIGYNGTAAGAPADWGSRYGVSSSECSQLPSGLQAGCOMRPFDFON 140
Qy 312 NSDNPMTFKEVTCPAELTTRSGCER 337
Db 197 NADNPSFSPFOVCCPAELVARTGCR 222

Search completed: June 18, 2003, 17:14:25
Job time : 29.3382 secs